

SEQUENCE LISTING

<110> Terrett, Jonathan A

<120> Protein Involved in Cancer

<130> 2543-1-038PCT/US

<140> PCT/GB2003/001589

<141> 2003-04-11

<150> GB0208332.7

<151> 2002-04-11

<150> GB0229875.0

<151> 2002-12-21

<160> 6

<170> PatentIn version 3.1

<210> 1

<211> 1212

<212> PRT

<213> Homo sapiens

<400> 1

Met	Glu	Pro	Arg	Pro	Thr	Ala	Pro	Ser	Ser	Gly	Ala	Pro	Gly	Leu	Ala
1				5					10					15	

Gly	Val	Gly	Glu	Thr	Pro	Ser	Ala	Ala	Ala	Leu	Ala	Ala	Ala	Arg	Val
			20				25						30		

Glu	Leu	Pro	Gly	Thr	Ala	Val	Pro	Ser	Val	Pro	Glu	Asp	Ala	Ala	Pro
		35					40					45			

Ala	Ser	Arg	Asp	Gly	Gly	Gly	Val	Arg	Asp	Glu	Gly	Pro	Ala	Ala	Ala
	50					55					60				

Gly	Asp	Gly	Leu	Gly	Arg	Pro	Leu	Gly	Pro	Thr	Pro	Ser	Gln	Ser	Arg
65					70					75					80

Phe	Gln	Val	Asp	Leu	Val	Ser	Glu	Asn	Ala	Gly	Arg	Ala	Ala	Ala	Ala
				85					90					95	

Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Gly	Ala	Gly	Ala	Gly
			100					105					110		

Ala	Lys	Gln	Thr	Pro	Ala	Asp	Gly	Glu	Ala	Ser	Gly	Glu	Ser	Glu	Pro	115	120	125
Ala	Lys	Gly	Ser	Glu	Glu	Ala	Lys	Gly	Arg	Phe	Arg	Val	Asn	Phe	Val	130	135	140
Asp	Pro	Ala	Ala	Ser	Ser	Ser	Ala	Glu	Asp	Ser	Leu	Ser	Asp	Ala	Ala	145	150	155
Gly	Val	Gly	Val	Asp	Gly	Pro	Asn	Val	Ser	Phe	Gln	Asn	Gly	Gly	Asp	165	170	175
Thr	Val	Leu	Ser	Glu	Gly	Ser	Ser	Leu	His	Ser	Gly	Gly	Gly	Gly	Gly	180	185	190
Ser	Gly	His	His	Gln	His	Tyr	Tyr	Tyr	Asp	Thr	His	Thr	Asn	Thr	Tyr	195	200	205
Tyr	Leu	Arg	Thr	Phe	Gly	His	Asn	Thr	Met	Asp	Ala	Val	Pro	Arg	Ile	210	215	220
Asp	His	Tyr	Arg	His	Thr	Ala	Ala	Gln	Leu	Gly	Glu	Lys	Leu	Leu	Arg	225	230	235
Pro	Ser	Leu	Ala	Glu	Leu	His	Asp	Glu	Leu	Glu	Lys	Glu	Pro	Phe	Glu	245	250	255
Asp	Gly	Phe	Ala	Asn	Gly	Glu	Glu	Ser	Thr	Pro	Thr	Arg	Asp	Ala	Val	260	265	270
Val	Thr	Tyr	Thr	Ala	Glu	Ser	Lys	Gly	Val	Val	Lys	Phe	Gly	Trp	Ile	275	280	285
Lys	Gly	Val	Leu	Val	Arg	Cys	Met	Leu	Asn	Ile	Trp	Gly	Val	Met	Leu	290	295	300
Phe	Ile	Arg	Leu	Ser	Trp	Ile	Val	Gly	Gln	Ala	Gly	Ile	Gly	Leu	Ser	305	310	315
Val	Leu	Val	Ile	Met	Met	Ala	Thr	Val	Val	Thr	Thr	Ile	Thr	Gly	Leu	325	330	335
Ser	Thr	Ser	Ala	Ile	Ala	Thr	Asn	Gly	Phe	Val	Arg	Gly	Gly	Gly	Ala	340	345	350
Tyr	Tyr	Leu	Ile	Ser	Arg	Ser	Leu	Gly	Pro	Glu	Phe	Gly	Gly	Ala	Ile	355	360	365

Gly	Leu	Ile	Phe	Ala	Phe	Ala	Asn	Ala	Val	Ala	Val	Ala	Met	Tyr	Val	
370						375					380					
Val	Gly	Phe	Ala	Glu	Thr	Val	Val	Glu	Leu	Leu	Lys	Glu	His	Ser	Ile	
385					390					395					400	
Leu	Met	Ile	Asp	Glu	Ile	Asn	Asp	Ile	Arg	Ile	Ile	Gly	Ala	Ile	Thr	
				405					410					415		
Val	Val	Ile	Leu	Leu	Gly	Ile	Ser	Val	Ala	Gly	Met	Glu	Trp	Glu	Ala	
			420					425					430			
Lys	Ala	Gln	Ile	Val	Leu	Leu	Val	Ile	Leu	Leu	Leu	Ala	Ile	Gly	Asp	
		435					440					445				
Phe	Val	Ile	Gly	Thr	Phe	Ile	Pro	Leu	Glu	Ser	Lys	Lys	Pro	Lys	Gly	
450						455					460					
Phe	Phe	Gly	Tyr	Lys	Ser	Glu	Ile	Phe	Asn	Glu	Asn	Phe	Gly	Pro	Asp	
465					470					475					480	
Phe	Arg	Glu	Glu	Glu	Thr	Phe	Phe	Ser	Val	Phe	Ala	Ile	Phe	Phe	Pro	
				485					490					495		
Ala	Ala	Thr	Gly	Ile	Leu	Ala	Gly	Ala	Asn	Ile	Ser	Gly	Asp	Leu	Ala	
			500					505					510			
Asp	Pro	Gln	Ser	Ala	Ile	Pro	Lys	Gly	Thr	Leu	Leu	Ala	Ile	Leu	Ile	
		515					520					525				
Thr	Thr	Leu	Val	Tyr	Val	Gly	Ile	Ala	Val	Ser	Val	Gly	Ser	Cys	Val	
530						535					540					
Val	Arg	Asp	Ala	Thr	Gly	Asn	Val	Asn	Asp	Thr	Ile	Val	Thr	Glu	Leu	
545					550					555					560	
Thr	Asn	Cys	Thr	Ser	Ala	Ala	Cys	Lys	Leu	Asn	Phe	Asp	Phe	Ser	Ser	
				565					570					575		
Cys	Glu	Ser	Ser	Pro	Cys	Ser	Tyr	Gly	Leu	Met	Asn	Asn	Phe	Gln	Val	
			580					585					590			
Met	Ser	Met	Val	Ser	Gly	Phe	Thr	Pro	Leu	Ile	Ser	Ala	Gly	Ile	Phe	
		595					600					605				
Ser	Ala	Thr	Leu	Ser	Ser	Ala	Leu	Ala	Ser	Leu	Val	Ser	Ala	Pro	Lys	
610						615					620					

Ile	Phe	Gln	Ala	Leu	Cys	Lys	Asp	Asn	Ile	Tyr	Pro	Ala	Phe	Gln	Met	625	630	635	640
Phe	Ala	Lys	Gly	Tyr	Gly	Lys	Asn	Asn	Glu	Pro	Leu	Arg	Gly	Tyr	Ile	645	650	655	
Leu	Thr	Phe	Leu	Ile	Ala	Leu	Gly	Phe	Ile	Leu	Ile	Ala	Glu	Leu	Asn	660	665	670	
Val	Ile	Ala	Pro	Ile	Ile	Ser	Asn	Phe	Phe	Leu	Ala	Ser	Tyr	Ala	Leu	675	680	685	
Ile	Asn	Phe	Ser	Val	Phe	His	Ala	Ser	Leu	Ala	Lys	Ser	Pro	Gly	Trp	690	695	700	
Arg	Pro	Ala	Phe	Lys	Tyr	Tyr	Asn	Met	Trp	Ile	Ser	Leu	Leu	Gly	Ala	705	710	715	720
Ile	Leu	Cys	Cys	Ile	Val	Met	Phe	Val	Ile	Asn	Trp	Trp	Ala	Ala	Leu	725	730	735	
Leu	Thr	Tyr	Val	Ile	Val	Leu	Gly	Leu	Tyr	Ile	Tyr	Val	Thr	Tyr	Lys	740	745	750	
Lys	Pro	Asp	Val	Asn	Trp	Gly	Ser	Ser	Thr	Gln	Ala	Leu	Thr	Tyr	Leu	755	760	765	
Asn	Ala	Leu	Gln	His	Ser	Ile	Arg	Leu	Ser	Gly	Val	Glu	Asp	His	Val	770	775	780	
Lys	Asn	Phe	Arg	Pro	Gln	Cys	Leu	Val	Met	Thr	Gly	Ala	Pro	Asn	Ser	785	790	795	800
Arg	Pro	Ala	Leu	Leu	His	Leu	Val	His	Asp	Phe	Thr	Lys	Asn	Val	Gly	805	810	815	
Leu	Met	Ile	Cys	Gly	His	Val	His	Met	Gly	Pro	Arg	Arg	Gln	Ala	Met	820	825	830	
Lys	Glu	Met	Ser	Ile	Asp	Gln	Ala	Lys	Tyr	Gln	Arg	Trp	Leu	Ile	Lys	835	840	845	
Asn	Lys	Met	Lys	Ala	Phe	Tyr	Ala	Pro	Val	His	Ala	Asp	Asp	Leu	Arg	850	855	860	
Glu	Gly	Ala	Gln	Tyr	Leu	Met	Gln	Ala	Ala	Gly	Leu	Gly	Arg	Met	Lys	865	870	875	880

Pro	Asn	Thr	Leu	Val	Leu	Gly	Phe	Lys	Lys	Asp	Trp	Leu	Gln	Ala	Asp	
				885					890					895		
Met	Arg	Asp	Val	Asp	Met	Tyr	Ile	Asn	Leu	Phe	His	Asp	Ala	Phe	Asp	
			900					905					910			
Ile	Gln	Tyr	Gly	Val	Val	Val	Ile	Arg	Leu	Lys	Glu	Gly	Leu	Asp	Ile	
		915					920					925				
Ser	His	Leu	Gln	Gly	Gln	Glu	Glu	Leu	Leu	Ser	Ser	Gln	Glu	Lys	Ser	
	930					935					940					
Pro	Gly	Thr	Lys	Asp	Val	Val	Val	Ser	Val	Glu	Tyr	Ser	Lys	Lys	Ser	
945					950					955					960	
Asp	Leu	Asp	Thr	Ser	Lys	Pro	Leu	Ser	Glu	Lys	Pro	Ile	Thr	His	Lys	
				965					970					975		
Val	Glu	Glu	Glu	Asp	Gly	Lys	Thr	Ala	Thr	Gln	Pro	Leu	Leu	Lys	Lys	
			980					985					990			
Glu	Ser	Lys	Gly	Pro	Ile	Val	Pro	Leu	Asn	Val	Ala	Asp	Gln	Lys	Leu	
		995					1000					1005				
Leu	Glu	Ala	Ser	Thr	Gln	Phe	Gln	Lys	Lys	Gln	Gly	Lys	Asn	Thr		
	1010					1015					1020					
Ile	Asp	Val	Trp	Trp	Leu	Phe	Asp	Asp	Gly	Gly	Leu	Thr	Leu	Leu		
	1025					1030					1035					
Ile	Pro	Tyr	Leu	Leu	Thr	Thr	Lys	Lys	Lys	Trp	Lys	Asp	Cys	Lys		
	1040					1045					1050					
Ile	Arg	Val	Phe	Ile	Gly	Gly	Lys	Ile	Asn	Arg	Ile	Asp	His	Asp		
	1055					1060					1065					
Arg	Arg	Ala	Met	Ala	Thr	Leu	Leu	Ser	Lys	Phe	Arg	Ile	Asp	Phe		
	1070					1075					1080					
Ser	Asp	Ile	Met	Val	Leu	Gly	Asp	Ile	Asn	Thr	Lys	Pro	Lys	Lys		
	1085					1090					1095					
Glu	Asn	Ile	Ile	Ala	Phe	Glu	Glu	Ile	Ile	Glu	Pro	Tyr	Arg	Leu		
	1100					1105					1110					
His	Glu	Asp	Asp	Lys	Glu	Gln	Asp	Ile	Ala	Asp	Lys	Met	Lys	Glu		
	1115					1120					1125					

Asp Glu Pro Trp Arg Ile Thr Asp Asn Glu Leu Glu Leu Tyr Lys
1130 1135 1140

Thr Lys Thr Tyr Arg Gln Ile Arg Leu Asn Glu Leu Leu Lys Glu
1145 1150 1155

His Ser Ser Thr Ala Asn Ile Ile Val Met Ser Leu Pro Val Ala
1160 1165 1170

Arg Lys Gly Ala Val Ser Ser Ala Leu Tyr Met Ala Trp Leu Glu
1175 1180 1185

Ala Leu Ser Lys Asp Leu Pro Pro Ile Leu Leu Val Arg Gly Asn
1190 1195 1200

His Gln Ser Val Leu Thr Phe Tyr Ser
1205 1210

<210> 2

<211> 4098

<212> DNA

<213> Homo sapiens

1<400> 2

ggtggcctct gtggccgtcc aggctagcgg cggcccgag gcggcgggga gaaagactct
60

ctcacctggg cttgcggctg tggccaccgc cggccagggg tgtggagggc gtgctgccgg
120

agacgtccgc cgggctctgc agttccgccg ggggtcgggc agctatggag ccgcggccca
180

cggcgccctc ctccggcgcc ccgggactgg ccggggtcgg ggagacgccg tcagccgctg
240

cgctggccgc agccagggtg gaactgcccg gcacggctgt gccctcgggtg ccggaggatg
300

ctgcgcccgc gagccgggac ggcggcgggg tccgcgatga gggccccgcg gcggccgggg
360

acgggctggg cagacccttg gggcccaccc cgagccagag ccgtttccag gtggacctgg
420

tttccgagaa cgccgggcgg gccgctgctg cggcggcggc ggcggcggcg gcagcggcgg
480

cggtggtgc tggggcgggg gccaaagcaga cccccgcgga cggggaagcc agcggcgaga
540

gcgagccagc taaaggcagc gaggaagcca agggccgctt ccgcgtgaac ttcgtggacc
600

cagctgcctc ctcgtcggct gaagacagcc tgtcagatgc tgccgggggc ggagtcgacg
660

ggcccaacgt gagcttccag aacggcgggg acacggtgct gagcgagggc agcagcctgc
720

actccggcgg cggcggcggc agtgggcacc accagcacta ctattatgat acccacacca
780

acacctacta cctgcgcacc ttcggccaca acaccatgga cgctgtgccc aggatcgatc
840

actaccggca cacagccgcg cagctgggcg agaagctgct ccggcctagc ctggcggagc
900

tccacgacga gctggaaaag gaaccttttg aggatggctt tgcaaattggg gaagaaagta
960

ctccaaccag agatgctgtg gtcacgtata ctgcagaaag taaaggagtc gtgaagtttg
1020

gctggatcaa ggggtgtatta gtacgttgta tgttaaacad ttgggggtgtg atgcttttca
1080

ttagattgtc atggattgtg ggtcaagctg gaataggctc atcagtcctt gtaataatga
1140

tggccactgt tgtgacaact atcacaggat tgtctacttc agcaatagca actaatggat
1200

ttgtaagagg aggaggagca tattatttaa tatctagaag tctagggcca gaatttggtg
1260

gtgcaattgg tctaattctc gcctttgccca acgctgttgc agttgctatg tatgtgggtg
1320

gatttgcaga aaccgtgggtg gagttgctta aggaacattc catacttatg atagatgaaa
1380

tcaatgatat ccgaattatt ggagccatta cagtcgtgat tcttttaggt atctcagtag
1440

ctggaatgga gtgggaagca aaagctcaga ttgttctttt ggtgattcta cttcttgcta
1500

ttggtgattt cgtcatagga acatttatcc cactggagag caagaagcca aaagggtttt
1560

ttggttataa atctgaaata tttaatgaga actttgggcc cgattttcga gaggaagaga
1620

ctttcttttc tgtatttgcc atcttttttc ctgctgcaac tggatttctg gctggagcaa
1680

atatctcagg tgatcttgca gatcctcagt cagccatacc caaaggaaca ctctagcca
1740

ttttaattac tacattgggtt tacgtaggaa ttgcagtatc tgtaggttct tgtgttggtc
1800

gagatgccac tggaaacggt aatgacacta tcgtaacaga gctaacaaac tgtacttctg
1860

cagcctgcaa attaaacttt gatttttcat cttgtgaaag cagtccttgt tcctatggcc
1920

taatgaacaa cttccaggta atgagtatgg tgtcaggatt tacaccacta atttctgcag
1980

gtatattttc agccactctt tcttcagcat tagcatccct agtgagtgct cccaaaatat
2040

ttcaggctct atgtaaggac aacatctacc cagctttcca gatgtttgct aaaggttatg
2100

ggaaaaataa tgaacctctt cgtggctaca tcttaacatt ctttaattgca cttggattca
2160

tcttaattgc tgaactgaat gttattgcac caattatctc aaacttcttc cttgcatcat
2220

atgcattgat caatttttca gtattccatg catcacttgc aaaatctcca ggatggcgtc
2280

ctgcattcaa atactacaac atgtggatat cacttcttgg agcaattctt tgttgcatag
2340

taatgttcgt cattaaactgg tgggctgcat tgctaacata tgtgatagtc cttgggctgt
2400

atatttatgt tacctacaaa aaaccagatg tgaattgggg atcctctaca caagccctga
2460

cttacctgaa tgcactgcag cattcaattc gtctttctgg agtggaagac cacgtgaaaa
2520

actttaggcc acagtgtctt gttatgacag gtgctccaaa ctcacgtcca gctttacttc
2580

atcttgttca tgatttcaca aaaaatgttg gtttgatgat ctgtggccat gtacatatgg
2640

gtcctcgaag acaagccatg aaagagatgt ccatcgatca agccaaatat cagcgatggc
2700

ttattaagaa caaaatgaag gcattttatg ctccagtaca tgcagatgac ttgagagaag
2760

gtgcacagta tttgatgcag gctgctggtc ttggctgtat gaagccaaac acacttgtcc
2820

ttggatttaa gaaagattgg ttgcaagcag atatgaggga tgtggatatg tatataaact
2880

tattttcatga tgcttttgac atacaatatg gagtagtggt tattcgcccta aaagaaggtc
2940

tggatatatc tcatcttcaa ggacaagaag aattattgtc atcacaagag aaatctcctg
3000

gcaccaagga tgtggtagta agtgtggaat atagtaaaaa gtccgattta gatacttcca
3060

aaccactcag tgaaaaacca attacacaca aagttgagga agaggatggc aagactgcaa
3120

ctcaaccact gttgaaaaaa gaatccaaag gccctattgt gcctttaaat gtagctgacc
3180

aaaagcttct tgaagctagt acacagtttc agaaaaaaca aggaaagaat actattgatg
3240

tctggtggtt ttttgatgat ggaggtttga ccttattgat accttacctt ctgacgacca
3300

agaaaaaatg gaaagactgt aagatcagag tattcattgg tggaaagata aacagaatag
3360

accatgaccg gagagcgatg gctactttgc ttagcaagtt ccggatagac ttttctgata
3420

tcattggttct aggagatatc aataccaaac caaagaaaga aatatattata gcttttgagg
3480

aaatcattga gccatacaga cttcatgaag atgataaaga gcaagatatt gcagataaaa
3540

tgaagaaga tgaaccatgg cgaataacag ataatgagct tgaactttat aagaccaaga
3600

cataccggca gatcagggtta aatgagttat taaaggaaca ttcaagcaca gctaataatta
3660

ttgtcatgag tctcccagtt gcacgaaaag gtgctgtgtc tagtgctctc tacatggcat
3720

ggttagaagc tctatctaag gacctaccac caatcctcct agttcgtggg aatcatcaga
3780

gtgtccttac cttctattca taaatgttct atacagtga cagccctcca gaatgggtact
3840

tcagtgccta gtgtagtaac ctgaaatctt caatgacaca ttaacatcac aatggcgaat
3900

ggtgactttt ctttcacgat ttcattaatt tgaagcaca caggaaagct tgctccattg
3960

ataacgtgta tggagacttc ggttttagtc aattccatat ctcaatctta atgggtgattc
4020

ttctctgttg aactgaagtt tgtgagagta gttttccttt gctacttgaa tagcaataaa
4080

agcgtgttaa ctttttgg
4098

<210> 3
<211> 22
<212> DNA
<213> Artificial sequence
1<220>
<223> Primer
<400> 3
cacctactac ctgcgcacct tc
22

<210> 4
<211> 22
<212> DNA
<213> Artificial sequence
1<220>
<223> Primer
<400> 4
gaccacagca tctctggttg ga
22

<210> 5
<211> 12
<212> PRT
<213> Artificial sequence
1<220>
<223> synthetic peptide
<400> 5

Ser Lys Lys Pro Lys Gly Phe Phe Gly Tyr Lys Cys
1 5 10

<210> 6
<211> 16
<212> PRT
<213> Artificial sequence
1<220>
<223> synthetic peptide
<400> 6

Ser Gly Glu Ser Glu Pro Ala Lys Gly Ser Glu Glu Ala Lys Gly Cys
1 5 10 15